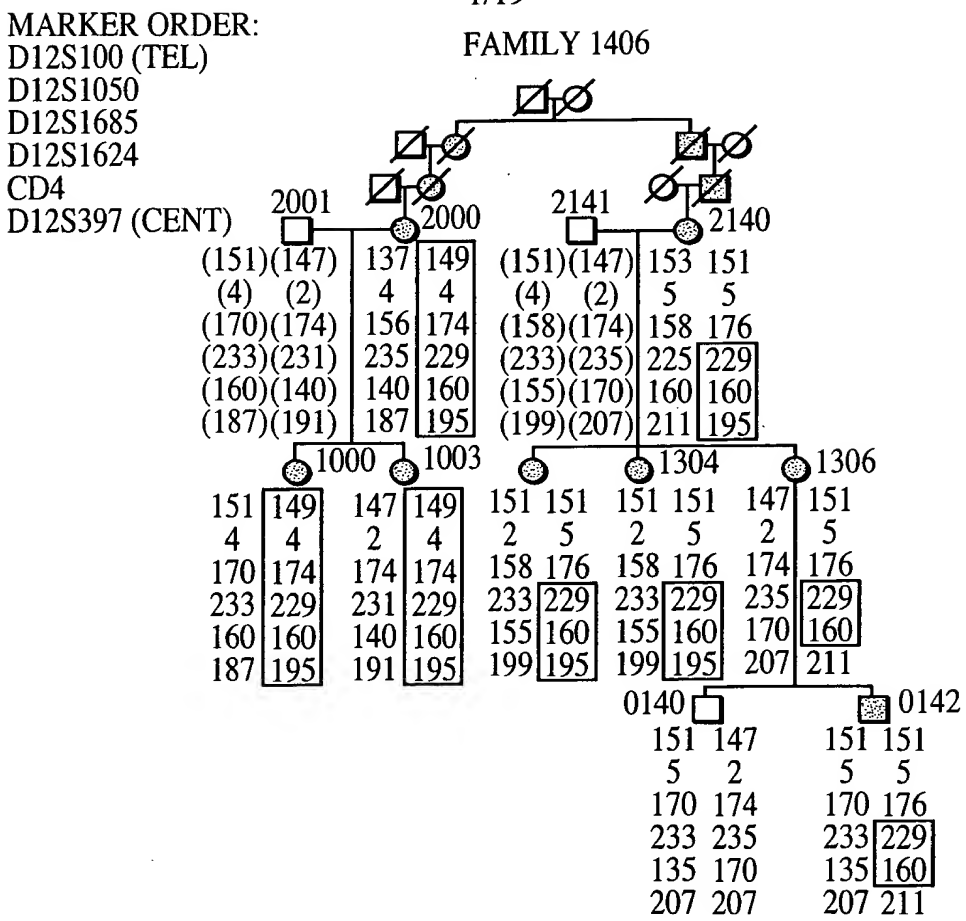
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D12S1050
D12S1685
D12S1624
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D12S397 (CENT)
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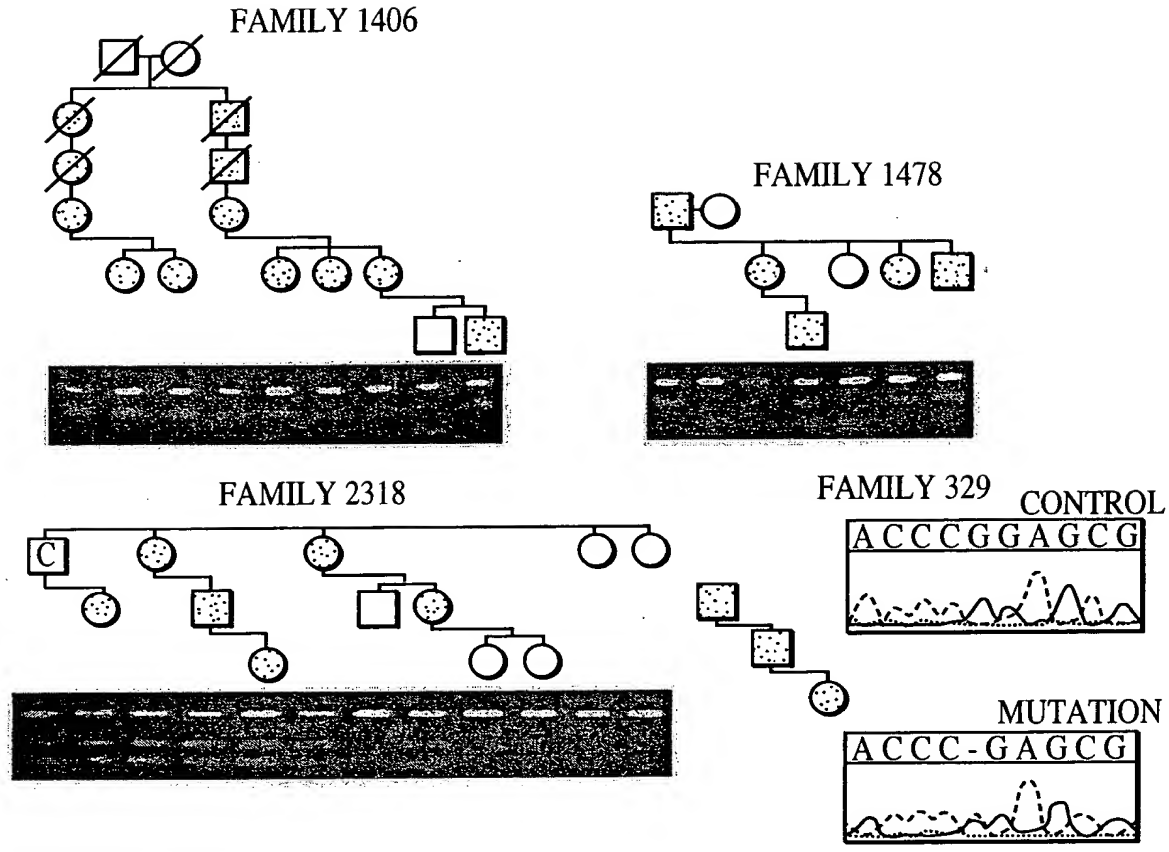
2001
2000
2141
2140
1000
1003
1304
1306
0140
0142
FAMILY 1478
MARKER ORDER:
D12S100 (TEL)
D12S1050
D12S1685
D12S1624
D12S1594
D12S397 (CENT)
1000
1001
0101
0102
0001
0100
9000

FIG. 1A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FAMILY 1478
FAMILY 2318
C
FAMILY 329
CONTROL
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MUTATION
ACCC-GAGCG

FIG. 1B

T007Z0"8E6T0660

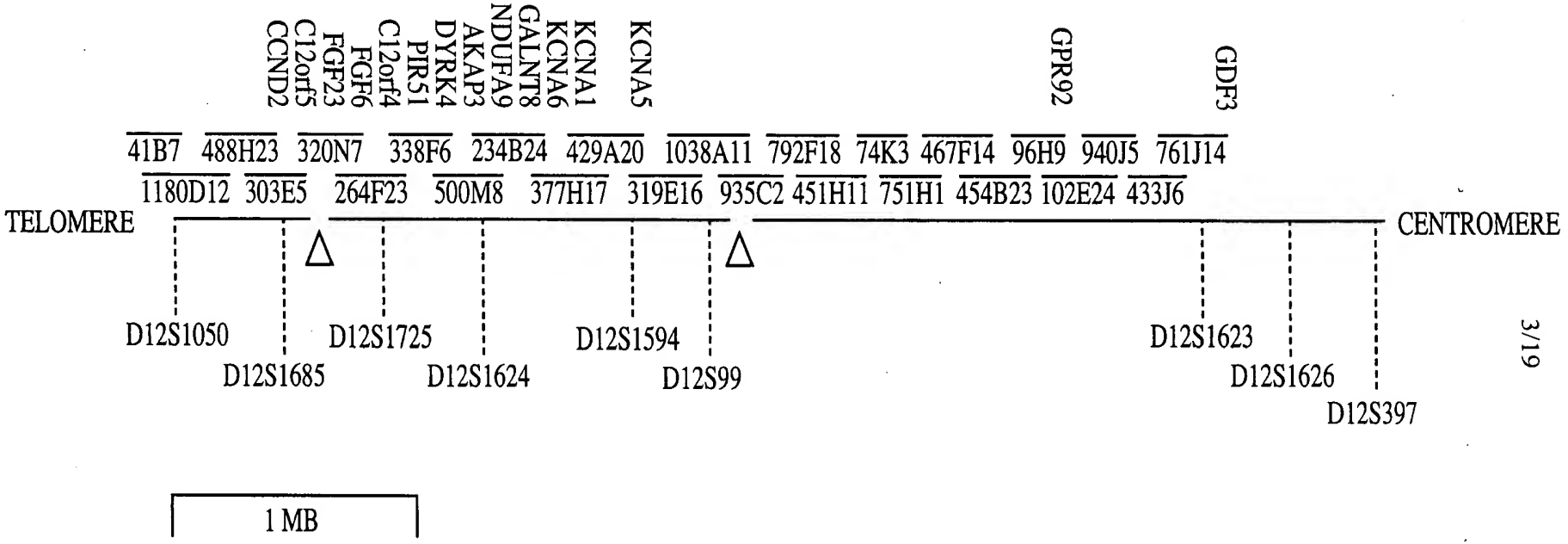
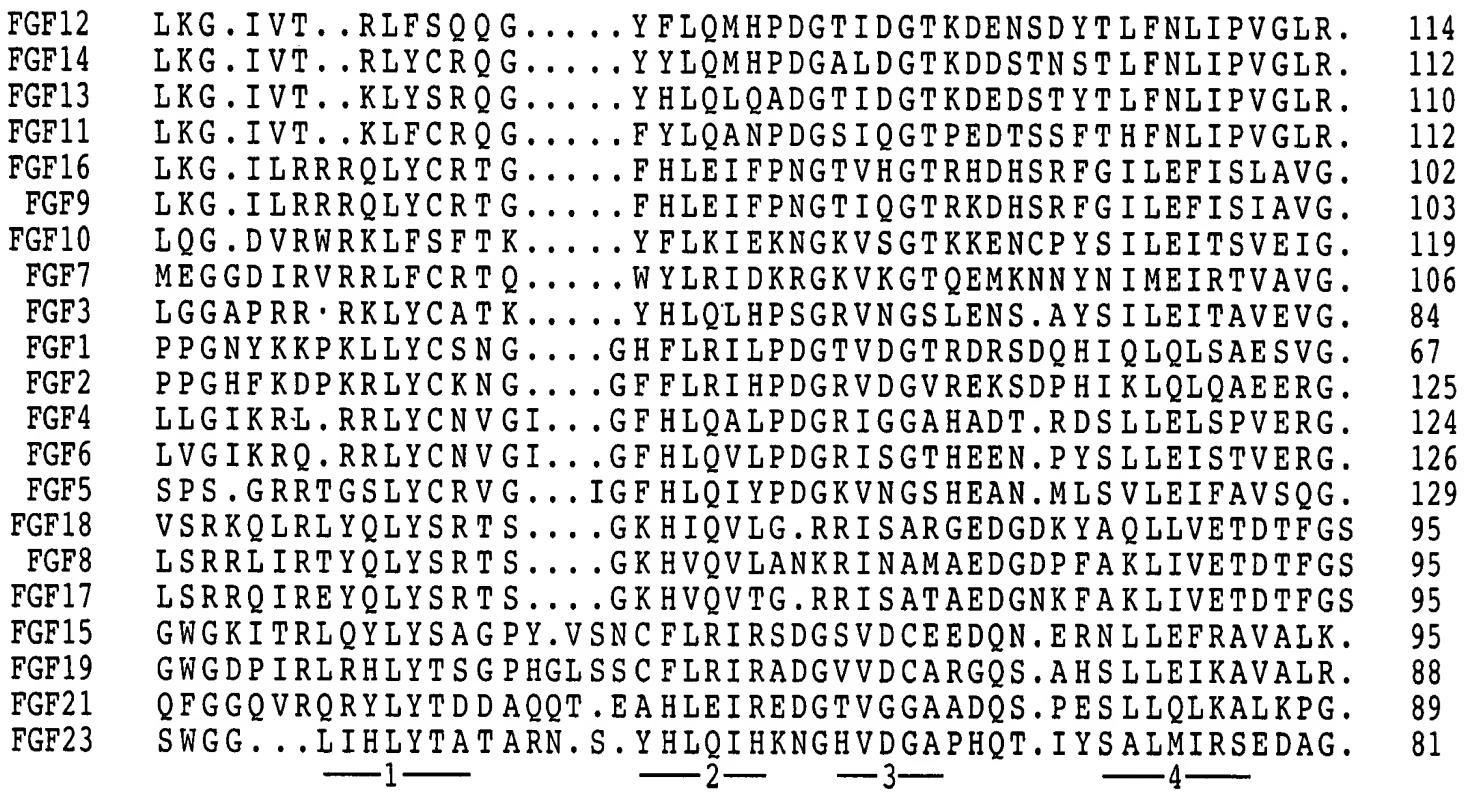


FIG. 2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FGF14 LKG.IVT..RLYCRQG.....YYLQMHPDGALDGTKDDSTNSTLFNLIPVGLR. 112
FGF13 LKG.IVT..KLYSRQG.....YHLQLQADGTIDGTKDEDSTYTLFNLIPVGLR. 110
FGF11 LKG.IVT..KLFCRQG.....FYLQANPDGSIQGTPEDTSSFTHFNLIPVGLR. 112
FGF16 LKG.ILRRRQLYCRTG.....FHLEIFPNGTVHGTRHDHSRFGILEFISLAVG. 102
FGF9 LKG.ILRRRQLYCRTG.....FHLEIFPNGTIQGTRKDHSRFGILEFISIAVG. 103
FGF10 LQG.DVRWRKLFSFTK.....YFLKIEKNGKVSGTKKENCPYSILEITSVEIG. 119
FGF7 MEGGDIRVRRLFCRTQ.....WYLRIDKRGKVKGTQEMKNNYNIMEIRTVAVG. 106
FGF3 LGGAPRR·RKLYCATK.....YHLQLHPSGRVNGSLENS.AYSILEITAVEVG. 84
FGF1 PPGNYKKPKLLYCSNG....GHFLRILPDGTVDGTRDRSDQHIQLQLSAESVG. 67
FGF2 PPGHFKDPKRLYCKNG....GFFLRIHPDGRVDGVREKSDPHIKLQLQAEERG. 125
FGF4 LLGIKRL.RRLYCNVGI...GFHLQALPDGRIGGAHADT.RDSLLELSPVERG. 124
FGF6 LVGIKRQ.RRLYCNVGI...GFHLQVLPDGRISGTHEEN.PYSLLEISTVERG. 126
FGF5 SPS.GRRTGSLYCRVG...IGFHLQIYPDGKVNGSHEAN.MLSVLEIFAVSQG. 129
FGF18 VSRKQLRLYQLYSRTS....GKHIQVLG.RRISARGEDGDKYAQLLVETDTFGS 95
FGF8 LSRRLIRTYQLYSRTS....GKHVQVLANKRINAMAEDGDPFAKLIVETDTFGS 95
FGF17 LSRRQIREYQLYSRTS....GKHVQVTG.RRISATAEDGNKFAKLIVETDTFGS 95
FGF15 GWGKITRLQYLYSAGPY.VSNCFLRIRSDGSVDCEEDQN.ERNLLEFRAVALK. 95
FGF19 GWGDPIRLRHLYTSGPHGLSSCFLRIRADGVVDCARGQS.AHSLLEIKAVALR. 88
FGF21 QFGGQVRQRYLYTDDAQQT.EAHLEIREDGTVGGAADQS.PESLLQLKALKPG. 89
FGF23 SWGG...LIHLYTATARN.S.YHLQIHKNGHVDGAPHQT.IYSALMIRSEDAG. 81
—1— —2— —3— —4—

FIG. 3A

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FGF14   VVAIQGVKTGLYIAMNGEGYLYPSEL.FTPECKFKESVFENYYVIYSSMLY...   162
FGF13   VVAIQGVQTKLYLAMNSEGYLYTSEL.FTPECKFKESVFENYYVTYSSMIY...   160
FGF11   VVTIQSAKLGHYMAMNAEGLLYSSPH.FTAECRFKECVFENYYVLYASALY...   162
FGF16   LISIRGVDSGLYLGMNERGELYGSKK.LTRECVFREQFEENWYNTYASTLY...   152
 FGF9   LVSIRGVDSGLYLGMNEKGELYGSEK.LTQECVFREQFEENWYNTYSSNLY...   153
FGF10   VVAVKAINSNYYLAMNKKGKLYGSKE.FNNDCKLKERIEENGYNTYASFNW...   169
 FGF7   IVAIKGVESEFYLAMNKEGKLYAKKE.CNEDCNFKELILENHYNTYASAKW...   156
 FGF3   IVAIRGLFSGRYLAMNKRGRLYASEH.YSAECEFVERIHELGYNTYASRLYRTV   137
 FGF1   EVYIKSTETGQYLAMDTDGLLYGSQT.PNEECLFLERLEENHYNTYISKKH...   117
 FGF2   VVSIKGVCANRYLAMKEDGRLLASKC.VTDECFFFERLESNNYNTYRSRKY...   175
 FGF4   VVSIFGVASRFFVAMSSKGKLYGSPF.FTDECTFKEILLPNNYNAYESYKY...   174
 FGF6   VVSLFGVRSALFVAMNSKGRLYATPS.FQEECKFRETLLPNNYNAYESDLY...   176
 FGF5   IVGIRGVFSNKFLAMSKKGKLHASAK.FTDDCKFRERFQENSYNTYASAIHRTE   182
FGF18   QVRIKGKETEFYLCMNRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAKY...   146
 FGF8   RVRVRGAETGLYICMNKKGKLIAKSNGKGKDCVFTEIVLENNYTALQNAKY...   146
FGF17   RVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLENNYTAFQNARH...   146
FGF15   TIAIKDVSSVRYLCMSADGKIYGLIRYSEEDCTFREEMDCLGYNQYRSMKH...   146
FGF19   TVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEEEIRPDGYNVYRSEKH...   139
FGF21   VIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH...   140
FGF23   FVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFL   135
        ——5——    ——6——   —7—        ——8——     ——9——
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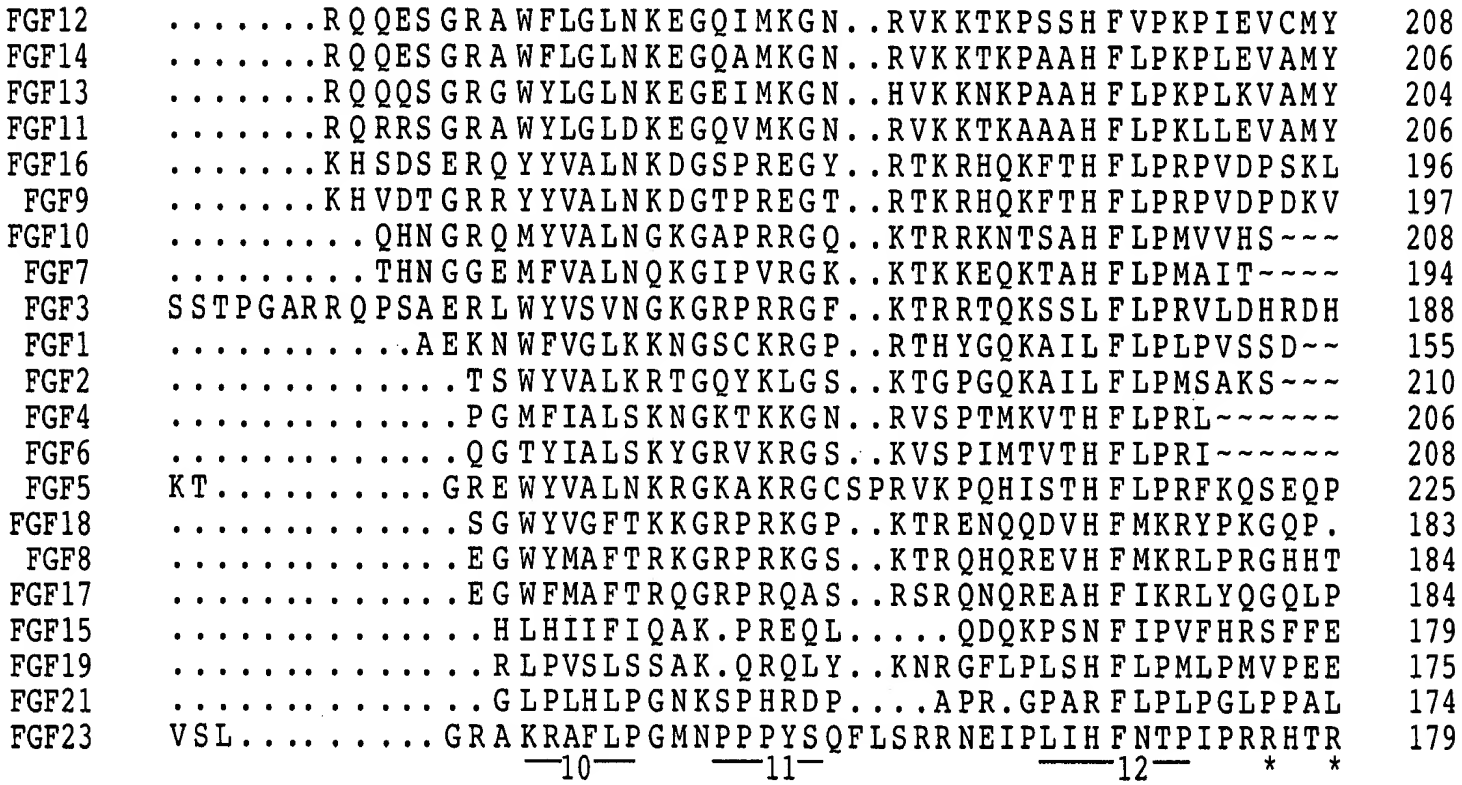
FIG. 3B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FGF13 .....RQQQSGRGWYLGLNKEGEIMKGN..HVKKNKPAAHFLPKPLKVAMY 204
FGF11 .....RQRRSGRAWYLGLDKEGQVMKGN..RVKKTKAAAHFLPKLLEVAMY 206
FGF16 .....KHSDSERQYYVALNKDGSPREGY..RTKRHQKFTHFLPRPVDPSKL 196
FGF9 .....KHVDTGRRYYVALNKDGTPREGT..RTKRHQKFTHFLPRPVDPDKV 197
FGF10 .....QHNGRQMYVALNGKGAPRRGQ..KTRRKNTSAHFLPMVVHS~~~ 208
FGF7 .....THNGGEMFVALNQKGIPVRGK..KTKKEQKTAHFLPMAIT~~~~ 194
FGF3 SSTPGARRQPSAERLWYVSVNGKGRPRRGF..KTRRTQKSSLFLPRVLDHRDH 188
FGF1 .....AEKNWFVGLKKNGSCKRGP..RTHYGQKAILFLPLPVSSD~~ 155
FGF2 .....TSWYVALKRTGQYKLGS..KTGPGQKAILFLPMSAKS~~~ 210
FGF4 .....PGMFIALSKNGKTKKGN..RVSPTMKVTHFLPRL~~~~~~ 206
FGF6 .....QGTYIALSKYGRVKRGS..KVSPIMTVTHFLPRI~~~~~~ 208
FGF5 KT.....GREWYVALNKRGKAKRGCSPRVKPQHISTHFLPRFKQSEQP 225
FGF18 .....SGWYVGFTKKGRPRKGP..KTRENQQDVHFMKRYPKGQP. 183
FGF8 .....EGWYMAFTRKGRPRKGS..KTRQHQREVHFMKRLPRGHHT 184
FGF17 .....EGWFMAFTRQGRPRQAS..RSRQNQREAHFIKRLYQGQLP 184
FGF15 .....HLHIIFIQAK.PREQL.....QDQKPSNFIPVFHRSFFE 179
FGF19 .....RLPVSLSSAK.QRQLY..KNRGFLPLSHFLPMLPMVPEE 175
FGF21 .....GLPLHLPGNKSPHRDP....APR.GPARFLPLPGLPPAL 174
FGF23 VSL.....GRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTR 179
10 11 12 * *

FIG. 3C

FIG. 4A

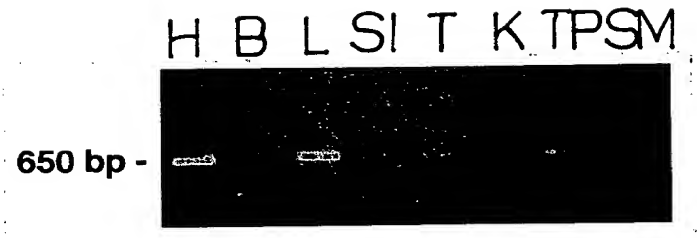

FIG. 4B

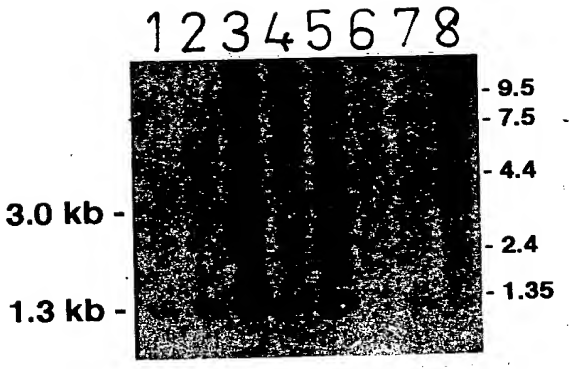

Figure 5A

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CAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGC
TCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAACA
GCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCA
TCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTT
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GAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTT
CCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAG
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GCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGAT
CCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC
GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGG
CCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGC
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CCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACCCTCTTTAACCC
ATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTC
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GTCATGGGGTTTCACCGCCTTCCTCACTCCATATAGAACACCTTTCCCA
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CCCGATCCCACTGGCATTTGAGTGTGCAAACCTTGACATTAACAGCTGA
ATGGGGCAAGTTGATGAAAACACTACTTTCAAGCCTTCGTTCTTCCTTG
AGCATCTCTGGGGAAGAGCTGTCAAAAGACTGGTGGTAGGCTGGTGAAA
ACTTGACAGCTAGACTTGATGCTTGCTGAAATGAGGCAGGAATCATAAT
AGAAAACTCAGCCTCCCTACAGGGTGAGCACCTTCTGTCTCGCT

EP 0 747 480 B1 09.08.2000

Figure 5B

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARN
SYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDF
RGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLP
GMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRSAEDDSERDPLNVLKPR
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PFAKFI

T00170.6E6T0660

Figure 6A

AGCCTGTCTGGGAGTGTCAGATTTCAAACTCAGCATTAGCCACTCAGTG
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TGCTTGGCTCCAACTGGGGAAGCCTGACCCACCTGTACACGGCTACAGC
CAGGACCAGCTATCACCTACAGATCCATAGGGATGGTCATGTAGATGGC
ACCCCCCATCAGACCATCTACAGTGCCCTGATGATTACATCAGAGGACG
CCGGCTCTGTGGTGATAACAGGAGCCATGACTCGAAGGTTCCTTTGTAT
GGATCTCCACGGCAACATTTTTGGATCGCTTCACTTCAGCCCAGAGAAT
TGCAAGTTCCGCCAGTGGACGCTGGAGAATGGCTATGACGTCTACTTGT
CGCAGAAGCATCACTACCTGGTGAGCCTGGGCCGCGCCAAGCGCATCTT
CCAGCCGGGCACCAACCCGCCGCCCTTCTCCCAGTTCCTGGCTCGCAGG
AACGAGGTCCCGCTGCTGCATTTCTACACTGTTCGCCCACGGCGCCACA
CGCGCAGCGCCGAGGACCCACCGGAGCGCGACCCACTGAACGTGCTCAA
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CGCCTCCATCCTCCAGTCGGTTCAGCCCACGTAGAGGAAGGACTAGGGT
ACCTCGAGGATGTCTGCTTCTCTCCCTTCCCTATGGGCCTGAGAGTCAC
CTGCGAGGTTCCAGCCAGGCACCGCTATTCAGAATTAAGAGCCAACGGT
GGGAGGCTGGAGAGGTGGCGCAGACAGTTCTCAGCACCCACAAATACCT
GTAATTCTAGCTCCAGGGGAATCTGTACTCACACACACACACATCCACA
CACACACACACACACATACATGTAATTTTAAATGTTAATCTGATTTAAA
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CATTTTAATCGATCAGTTAGCACGAGGAAAGAGTTCACGCCTTGAACAC
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GAAGAAAGACGCGCATTTCTTCTCTTTGGGAAGAGCTTTGGATTGGCGG
GAGGCTGACAAGGACACCTAAACCGAACACATTTCAGAGTTCAGCCTCC
CTGAGGAATGATTCGCCAATGATTCTGTGATAGGACCAGTCAGTAGCTT
TTGAATTTGCCCTGGCTCAGCAAAGTCTACCTTGCTAGGG

1004420.82600

Figure 6B

MLGTCLRLLVGVLCTVCSLGTARAYPDTSPLLGSNWGSLTHLYTATART
SYHLQIHRDGHVDGTPHQTIYSALMITSEDAGSVVITGAMTRRFLCMDL
HGNIFGSLHFSPENCKFRQWTLENGYDVYLSQKHHYLVSLGRAKRIFQP
GTNPPPFSQFLARRNEVPLLHFYTVRPRRHTRSAEDPPERDPLNVLKPR
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PFPRFV

FOOT/0-88938T0660

FIG. 7A

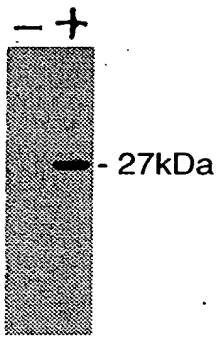


FIG. 7B

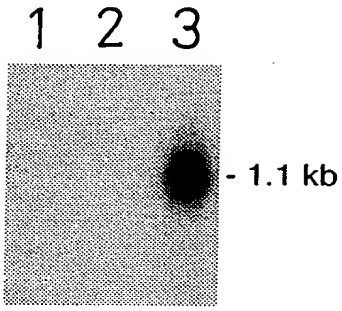


FIG. 7C

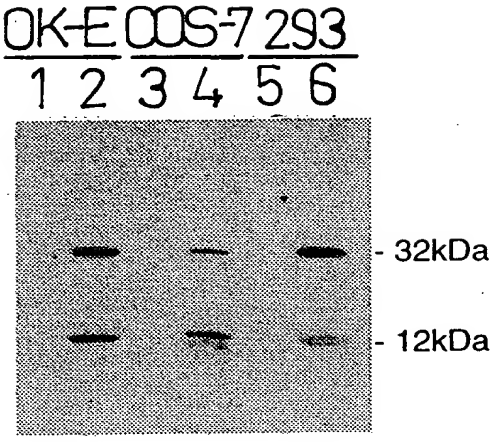


FIG. 8A

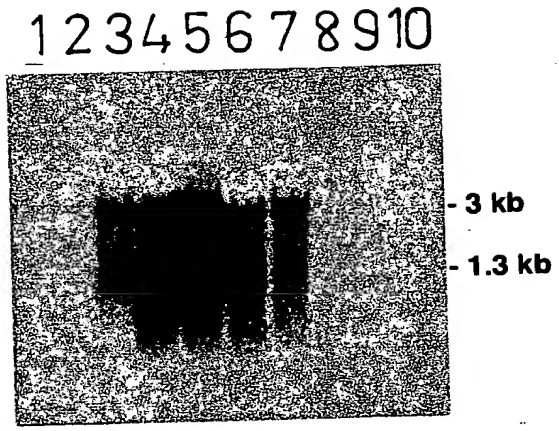
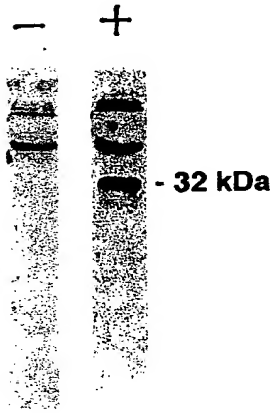


FIG. 8B



T00T20"3E6T0660

Figure 9

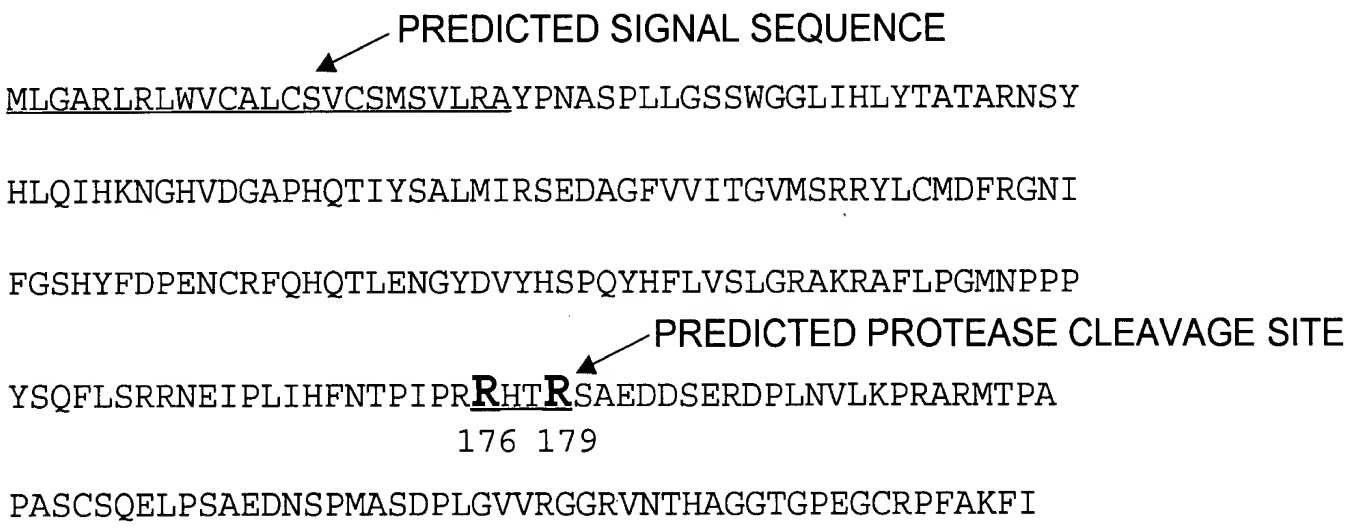


FIG. 10A

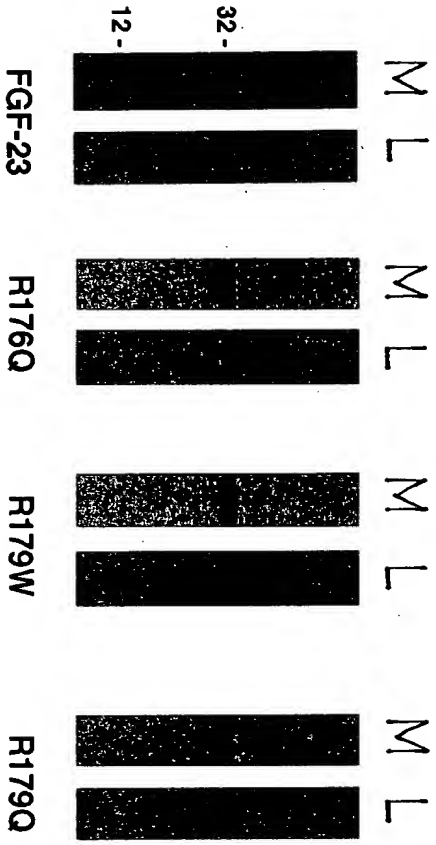
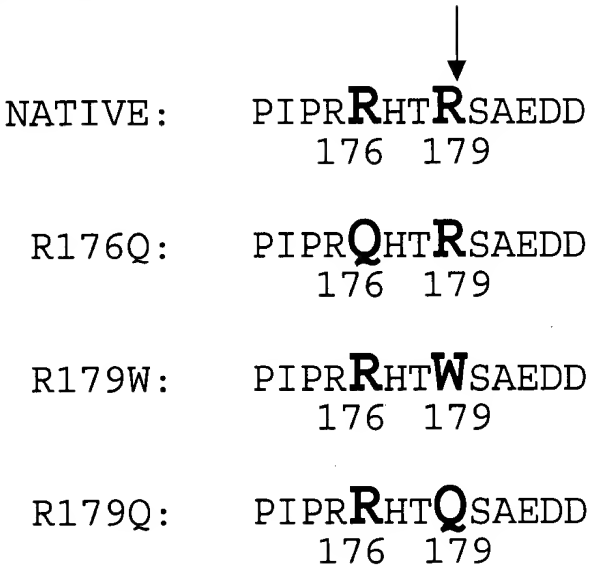


Figure 10B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R176Q: PIPRQHTRSAEDD
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R179Q: PIPRRHTQSAEDD
176 179

FIG. 11A

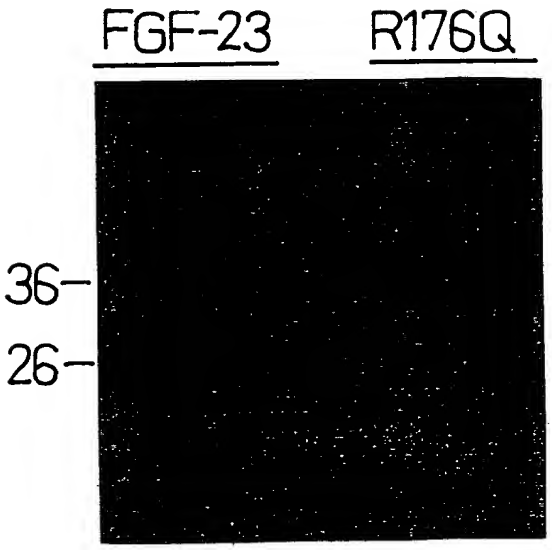
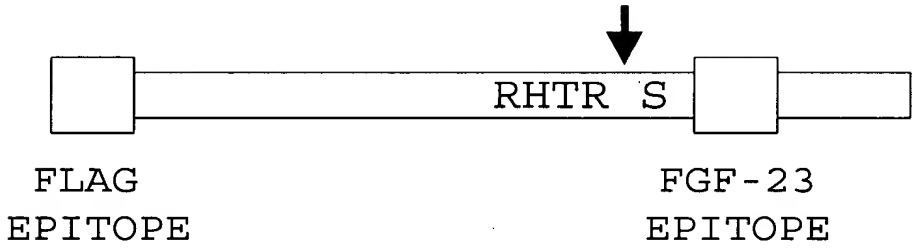


FIG. 11B



FOUR-POINT BEND

FIG. 12A

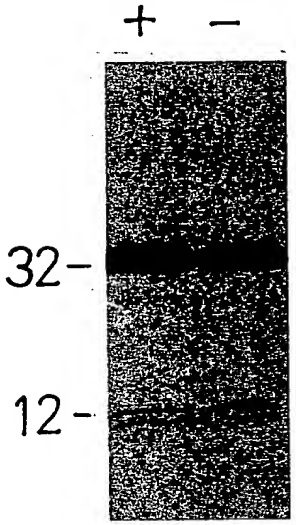


FIG. 12B

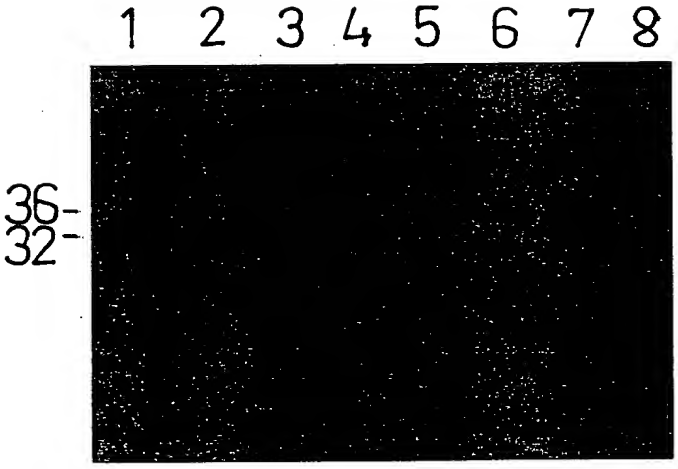



FIG. 13